GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 31, 2004, 08:15:31 ; Search time 3 Seconds
(without alignments)
2.895 Million cell updates/sec

Title: us-09-869-334b-2
Perfect score: 1191
Sequence: 1 atgaatgtgttaaaccgccg.....gcttccgtgtgaaaatgtaa 1191

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 3 seqs, 3646 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : sub.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1186.2	99.6	1204	1	US-09-869-334B-41	Sequence 41, Appl
2	1181.4	99.2	1221	1	US-09-869-334B-43	Sequence 43, Appl
3	1168.6	98.1	1221	1	US-09-869-334B-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-869-334B-41
; Sequence 41, Application US/09869334B
; GENERAL INFORMATION:
; APPLICANT: ENDO, Hirofumi
; APPLICANT: MIZOGUCHI, Hiroshi
; APPLICANT: OZAKI, Akio
; APPLICANT: YONETANI, Yoshiyuki
; APPLICANT: HASHIMOTO, Shin-ichi
; TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
; FILE REFERENCE: P21289
; CURRENT APPLICATION NUMBER: US/09/869,334B
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: PCT JP00/00472
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-09-869-334B-41

Query Match 99.6%; Score 1186.2; DB 1; Length 1204;
Best Local Similarity 99.7%; Pred. No. 0;

Matches 1188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 ATGAATGTGTTAAACCGCCGGCAAGCCTTGCAGCGAGCGCTGCTCAATGGGAAAAACAAA 60
Db       8 ATGAATGTGTTAAACCGCCGGCAAGCCTTGCAGCGAGCGCTGCTCAATGGGAAAAACAAA 67

Qy      61 CAGGATGCGTATCATCCGTTTCCATGGTATGAATCGATGAGAAAGGATGCGCCTGTTTCC 120
Db      68 CAGGATGCGTATCATCCGTTTCCATGGTATGAATCGATGAGAAAGGATGCGCCTGTTTCC 127

Qy     121 TTTGATGAAGAAAACCAAGTGTGGAGCGTTTTTCTTTATGATGATGTCAAAAAAGTTGTT 180
Db     128 TTTGATGAAGAAAACCAAGTGTGGAGCGTTTTTCTTTATGATGATGTCAAAAAAGTTGTT 187

Qy     181 GGGGATAAAGAGTTGTTTTCCAGTTGCATGCCGCAGCAGACAAGCTCTATTGGAAATTCC 240
Db     188 GGGGATAAAGAGTTGTTTTCCAGTTGCATGCCGCAGCAGACAAGCTCTATTGGAAATTCC 247

Qy     241 ATCATTAACATGGACCCGCCGAAGCATACAAAAATCCGTTCAGTCGTGAACAAAGCCTTT 300
Db     248 ATCATTAACATGGACCCGCCGAAGCATACAAAAATCCGTTCAGTCGTGAACAAAGCCTTT 307

Qy     301 ACTCCGCGCGTGATGAAGCAATGGGAACCGAGAATTCAAGAAATCACAGATGAACTGATT 360
Db     308 ACTCCGCGCGCGATGAAGCAATGGGAACCGAGAATTCAAGAAATCACAGATGAACTGATT 367

Qy     361 CAAAAATTTCAGGGGCGCAGTGAGTTTGACCTTGTTCACGATTTTTCATACCCGCTTCCG 420
Db     368 CAAAAATTTCAGGGGCGCAGTGAGTTTGACCTTGTTCACGATTTTTCATACCCGCTTCCG 427

Qy     421 GTTATTGTGATATCTGAGCTGCTGGGAGTGCCTTCAGCGCAGATGGAACAGTTTAAAGCA 480
Db     428 GTTATTGTGATATCTGAGCTGCTGGGAGTGCCTTCAGCGCATATGGAACAGTTTAAAGCA 487

Qy     481 TGGTCTGATCTTCTGGTCAGTACACCGAAGGATAAAAGTGAAGAAGCTGAAAAAGCCTTT 540
Db     488 TGGTCTGATCTTCTGGTCAGTACACCGAAGGATAAAAGTGAAGAAGCTGAAAAAGCCTTT 547

Qy     541 TTGGAAGAACGAGATAAGTGTGAGGAAGAACTGGCCGCGTTTTTTGCCGGCATCATAGAA 600
Db     548 TTGGAAGAACGAGATAAGTGTGAGGAAGAACTGGCCGCGTTTTTTGCCGGCATCATAGAA 607

Qy     601 GAAAAGCGAAACAAACCGGAACAGGATATTATTTCTATTTTAGTGGAAGCGGAAGAAACA 660
Db     608 GAAAAGCGAAACAAACCGGAACAGGATATTATTTCTATTTTAGTGGAAGCGGAAGAAACA 667

Qy     661 GGCGAGAAGCTGTCCGGTGAAGAGCTGATTCCGTTTTGCACGCTGCTGCTGGTGGCCGGA 720
Db     668 GGCGAGAAGCTGTCCGGTGAAGAGCTGATTCCGTTGTGCACGCTGCTGCTGGTGGCCGGA 727

Qy     721 AATGAAACCACTACAAACCTGATTTCAAATGCGATGTACAGCATATTAGAAACGCCAGGC 780
Db     728 AATGAAACCACTACAAACCTGATTTCAAATGCGATGTACAGCATATTAGAAACGCCAGGC 787

Qy     781 GTTTACGAGGAACTGCGCAGCCATCCTGAACTGATGCCTCAGGCAGTGGAGGAAGCCTTG 840
Db     788 GTTTACGAGGAACTGCGCAGCCATCCTGAACTGATGCCTCAGGCAGTGGAGGAAGCCTTG 847

Qy     841 CGTTTCAGAGCGCCGGCCCCGGTTTTGAGGCGCATTGCCAAGCGGGATACGGAGATCGGG 900
Db     848 CGTTTCAGAGCGCCGGCCCCGGTTTTGAGGCGCATTGCCAAGCGGGATACGGAGATCGGG 907

Qy     901 GGGCACCTGATTAAAGAAGGTGATATGGTTTTGGCGTTTGTGGCATCGGCAAATCGTGAT 960
Db     908 GGGCACCTGATTAAAGAAGGTGATATGGTTTTGGCGTTTGTGGCATCGGCAAATCGTGAT 967

Qy     961 GAAGCAAAGTTTGACAGACCGCACATGTTTGATATCCGCCGCCATCCCAATCCGCATATT 1020
Db     968 GAAGCAAAGTTTGACAGACCGCACATGTTTGATATCCGCCGCCATCCCAATCCGCATATT 1027

Qy    1021 GCGTTTGGCCACGGCATCCATTTTTGCCTTGGGGCCCCGCTTGCCCGTCTTGAAGCAAAT 1080
Db    1028 GCGTTTGGCCACGGCATCCATTTTTGCCTTGGGGCCCCGCTTGCCCGTCTTGAAGCAAAT 1087
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Qy       1081 ATCGCGTTAACGTCTTTGATTTCTGCTTTTCCTCATATGGAGTGCGTCAGTATCACTCCG 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 ATCGCGTTAACGTCTTTGATTTCTGCTTTTCCTCATATGGAGTGCGTCAGTATCACTCCG 1147

Qy       1141 ATTGAAAACAGTGTGATATACGGATTAAAGAGCTTCCGTGTGAAAATGTAA 1191
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1148 ATTGAAAACAGTGTGATATACGGATTAAAGAGCTTCCGTGTGAAAATGTAA 1198


RESULT 2
US-09-869-334B-43
; Sequence 43, Application US/09869334B
; GENERAL INFORMATION:
;  APPLICANT: ENDO, Hirofumi
;  APPLICANT:  MIZOGUCHI, Hiroshi
;  APPLICANT:  OZAKI, Akio
;  APPLICANT:  YONETANI, Yoshiyuki
;  APPLICANT:  HASHIMOTO, Shin-ichi
;  TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
;  FILE REFERENCE: P21289
;  CURRENT APPLICATION NUMBER: US/09/869,334B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: PCT JP00/00472
;  PRIOR FILING DATE: 2000-01-28
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 1221
;   TYPE: DNA
;   ORGANISM: Bacillus subtilis
US-09-869-334B-43

  Query Match             99.2%;  Score 1181.4;  DB 1;  Length 1221;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 1185;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGAATGTGTTAAACCGCCGGCAAGCCTTGCAGCGAGCGCTGCTCAATGGGAAAAACAAA 60
              |||||  ||   | ||||||| ||||||||||||||||||||||||||||||||||||
Db         25 ATGAACGTTCTGAACCGCCGTCAAGCCTTGCAGCGAGCGCTGCTCAATGGGAAAAACAAA 84

Qy         61 CAGGATGCGTATCATCCGTTTCCATGGTATGAATCGATGAGAAAGGATGCGCCTGTTTCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 CAGGATGCGTATCATCCGTTTCCATGGTATGAATCGATGAGAAAGGATGCGCCTGTTTCC 144

Qy        121 TTTGATGAAGAAAACCAAGTGTGGAGCGTTTTTCTTTATGATGATGTCAAAAAAGTTGTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 TTTGATGAAGAAAACCAAGTGTGGAGCGTTTTTCTTTATGATGATGTCAAAAAAGTTGTT 204

Qy        181 GGGGATAAAGAGTTGTTTTCCAGTTGCATGCCGCAGCAGACAAGCTCTATTGGAAATTCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GGGGATAAAGAGTTGTTTTCCAGTTGCATGCCGCAGCAGACAAGCTCTATTGGAAATTCC 264

Qy        241 ATCATTAACATGGACCCGCCGAAGCATACAAAAATCCGTTCAGTCGTGAACAAAGCCTTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 ATCATTAACATGGACCCGCCGAAGCATACAAAAATCCGTTCAGTCGTGAACAAAGCCTTT 324

Qy        301 ACTCCGCGCGTGATGAAGCAATGGGAACCGAGAATTCAAGAAATCACAGATGAACTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 ACTCCGCGCGTGATGAAGCAATGGGAACCGAGAATTCAAGAAATCACAGATGAACTGATT 384

Qy        361 CAAAAATTTCAGGGGCGCAGTGAGTTTGACCTTGTTCACGATTTTTCATACCCGCTTCCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CAAAAATTTCAGGGGCGCAGTGAGTTTGACCTTGTTCACGATTTTTCATACCCGCTTCCG 444

Qy        421 GTTATTGTGATATCTGAGCTGCTGGGAGTGCCTTCAGCGCAGATGGAACAGTTTAAAGCA 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GTTATTGTGATATCTGAGCTGCTGGGAGTGCCTTCAGCGCATATGGAACAGTTTAAAGCA 504

Qy        481 TGGTCTGATCTTCTGGTCAGTACACCGAAGGATAAAAGTGAAGAAGCTGAAAAAGCCTTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 TGGTCTGATCTTCTGGTCAGTACACCGAAGGATAAAAGTGAAGAAGCTGAAAAAGCCTTT 564

Qy        541 TTGGAAGAACGAGATAAGTGTGAGGAAGAACTGGCCGCGTTTTTTGCCGGCATCATAGAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 TTGGAAGAACGAGATAAGTGTGAGGAAGAACTGGCCGCGTTTTTTGCCGGCATCATAGAA 624

Qy        601 GAAAAGCGAAACAAACCGGAACAGGATATTATTTCTATTTTAGTGGAAGCGGAAGAAACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 GAAAAGCGAAACAAACCGGAACAGGATATTATTTCTATTTTAGTGGAAGCGGAAGAAACA 684

Qy        661 GGCGAGAAGCTGTCCGGTGAAGAGCTGATTCCGTTTTGCACGCTGCTGCTGGTGGCCGGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 GGCGAGAAGCTGTCCGGTGAAGAGCTGATTCCGTTTTGCACGCTGCTGCTGGTGGCCGGA 744

Qy        721 AATGAAACCACTACAAACCTGATTTCAAATGCGATGTACAGCATATTAGAAACGCCAGGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 AATGAAACCACTACAAACCTGATTTCAAATGCGATGTACAGCATATTAGAAACGCCAGGC 804

Qy        781 GTTTACGAGGAACTGCGCAGCCATCCTGAACTGATGCCTCAGGCAGTGGAGGAAGCCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 GTTTACGAGGAACTGCGCAGCCATCCTGAACTGATGCCTCAGGCAGTGGAGGAAGCCTTG 864

Qy        841 CGTTTCAGAGCGCCGGCCCCGGTTTTGAGGCGCATTGCCAAGCGGGATACGGAGATCGGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 CGTTTCAGAGCGCCGGCCCCGGTTTTGAGGCGCATTGCCAAGCGGGATACGGAGATCGGG 924

Qy        901 GGGCACCTGATTAAAGAAGGTGATATGGTTTTGGCGTTTGTGGCATCGGCAAATCGTGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 GGGCACCTGATTAAAGAAGGTGATATGGTTTTGGCGTTTGTGGCATCGGCAAATCGTGAT 984

Qy        961 GAAGCAAAGTTTGACAGACCGCACATGTTTGATATCCGCCGCCATCCCAATCCGCATATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 GAAGCAAAGTTTGACAGACCGCACATGTTTGATATCCGCCGCCATCCCAATCCGCATATT 1044

Qy       1021 GCGTTTGGCCACGGCATCCATTTTTGCCTTGGGGCCCCGCTTGCCCGTCTTGAAGCAAAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1045 GCGTTTGGCCACGGCATCCATTTTTGCCTTGGGGCCCCGCTTGCCCGTCTTGAAGCAAAT 1104

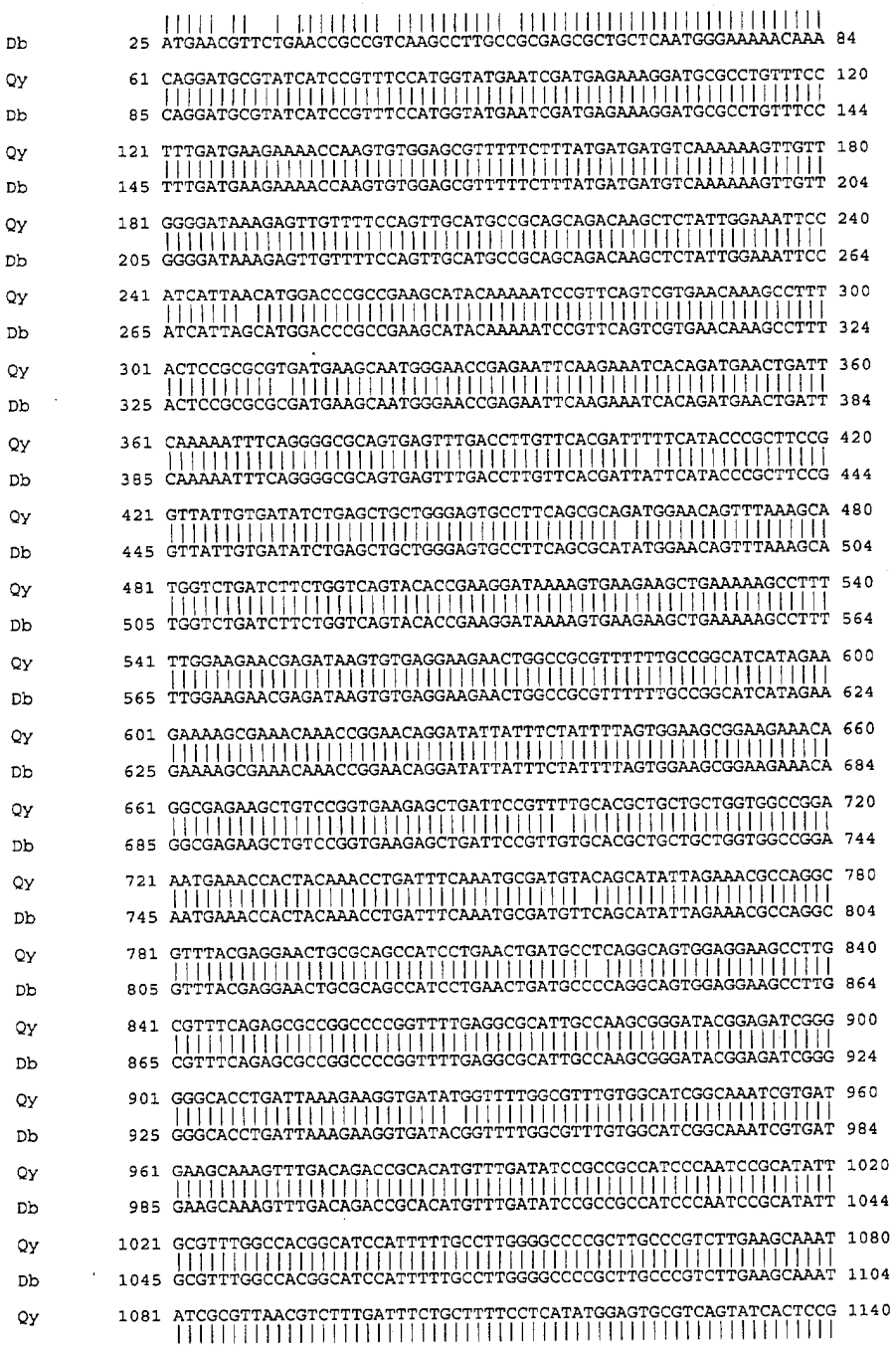
Qy       1081 ATCGCGTTAACGTCTTTGATTTCTGCTTTTCCTCATATGGAGTGCGTCAGTATCACTCCG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 ATCGCGTTAACGTCTTTGATTTCTGCTTTTCCTCATATGGAGTGCGTCAGTATCACTCCG 1164

Qy       1141 ATTGAAAACAGTGTGATATACGGATTAAAGAGCTTCCGTGTGAAAATGTAA 1191
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1165 ATTGAAAACAGTGTGATATACGGATTAAAGAGCTTCCGTGTGAAAATGTAA 1215


RESULT 3
US-09-869-334B-44
; Sequence 44, Application US/09869334B
; GENERAL INFORMATION:
;  APPLICANT: ENDO, Hirofumi
;  APPLICANT:  MIZOGUCHI, Hiroshi
;  APPLICANT:  OZAKI, Akio
;  APPLICANT:  YONETANI, Yoshiyuki
;  APPLICANT:  HASHIMOTO, Shin-ichi
;  TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
;  FILE REFERENCE: P21289
;  CURRENT APPLICATION NUMBER: US/09/869,334B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: PCT JP00/00472
;  PRIOR FILING DATE: 2000-01-28
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
;   LENGTH: 1221
;   TYPE: DNA
;   ORGANISM: Bacillus subtilis
US-09-869-334B-44

  Query Match             98.1%;  Score 1168.6;  DB 1;  Length 1221;
  Best Local Similarity   98.8%;  Pred. No. 0;
  Matches 1177;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 ATGAATGTGTTAAACCGCCGGCAAGCCTTGCAGCGAGCGCTGCTCAATGGGAAAAACAAA 60
```



Search completed: March 31, 2004, 08:15:34
Job time : 3 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 31, 2004, 08:11:35 ; Search time 0.001 Seconds
(without alignments)
313.632 Million cell updates/sec

Title: us-09-869-334b-1
Perfect score: 2052
Sequence: 1 MNVLNRRQALQRALLNGKNK.....SITPIENSVIYGLKSFRVKM 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 792 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : us-09-869-334b-4*:*
1: /home/sdavid/sdavid-tmp/mar04/ramirez334/us-09-869-334b-42:*
2: /home/sdavid/sdavid-tmp/mar04/ramirez334/us-09-869-334b-45:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2042	99.5	396	1	us-09-869-334b-42	
2	2018	98.3	396	2	us-09-869-334b-45	

ALIGNMENTS

RESULT 1
us-09-869-334b-42

Query Match 99.5%; Score 2042; DB 1; Length 396;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 394; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60

Qy         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRVMKQWEPRIQEITDELI 120
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRAMKQWEPRIQEITDELI 120

Qy        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180

Qy        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPFCTLLLVAG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPLCTLLLVAG 240

Qy        241 NETTTNLISNAMYSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NETTTNLISNAMYSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300

Qy        301 GHLIKEGDMVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GHLIKEGDMVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360

Qy        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396
              ||||||||||||||||||||||||||||||||||||
Db        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396
```

RESULT 2
us-09-869-334b-45

Query Match 98.3%; Score 2018; DB 2; Length 396;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 389; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNVLNRRQALPRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60

Qy         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRVMKQWEPRIQEITDELI 120
              |||||||||||||||||||||:|||||||||||||||||| ||||||||||||||||||
Db         61 GDKELFSSCMPQQTSSIGNSIISMDPPKHTKIRSVVNKAFTPRAMKQWEPRIQEITDELI 120

Qy        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKFQGRSEFDLVHDYSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180

Qy        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPFCTLLLVAG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPLCTLLLVAG 240

Qy        241 NETTTNLISNAMYSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300
              ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NETTTNLISNAMFSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300

Qy        301 GHLIKEGDMVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GHLIKEGDTVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360

Qy        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396
              ||||||||||||||||||||||||||||||||||||
Db        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396
```

Search completed: March 31, 2004, 08:11:36
Job time : 1 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 31, 2004, 08:08:52 ; Search time 0.001 Seconds
(without alignments)
470.448 Million cell updates/sec

Title: 2633575
Perfect score: 2052
Sequence: 1 mnvlnrrqalqrallngknk.....sitpiensviyglksfrvkm 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3 seqs, 1188 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : US09869334B.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2052	100.0	396	1	US-09-869-334B-1	Sequence 1, Appli
2	2042	99.5	396	1	US-09-869-334B-42	Sequence 42, Appl
3	2018	98.3	396	1	US-09-869-334B-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-869-334B-1
; Sequence 1, Application US/09869334B
; GENERAL INFORMATION:
; APPLICANT: ENDO, Hirofumi
; APPLICANT: MIZOGUCHI, Hiroshi
; APPLICANT: OZAKI, Akio
; APPLICANT: YONETANI, Yoshiyuki
; APPLICANT: HASHIMOTO, Shin-ichi
; TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
; FILE REFERENCE: P21289
; CURRENT APPLICATION NUMBER: US/09/869,334B
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: PCT JP00/00472
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-869-334B-1

Query Match 100.0%; Score 2052; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60

Qy         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRVMKQWEPRIQEITDELI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRVMKQWEPRIQEITDELI 120

Qy        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180

Qy        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPFCTLLLVAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPFCTLLLVAG 240

Qy        241 NETTTNLISNAMYSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NETTTNLISNAMYSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300

Qy        301 GHLIKEGDMVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GHLIKEGDMVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360

Qy        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396
              ||||||||||||||||||||||||||||||||||||
Db        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396
```

RESULT 2
US-09-869-334B-42
; Sequence 42, Application US/09869334B
; GENERAL INFORMATION:
; APPLICANT: ENDO, Hirofumi
; APPLICANT: MIZOGUCHI, Hiroshi
; APPLICANT: OZAKI, Akio
; APPLICANT: YONETANI, Yoshiyuki
; APPLICANT: HASHIMOTO, Shin-ichi
; TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
; FILE REFERENCE: P21289
; CURRENT APPLICATION NUMBER: US/09/869,334B
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: PCT JP00/00472
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-869-334B-42

Query Match 99.5%; Score 2042; DB 1; Length 396;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 394; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60

Qy         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRVMKQWEPRIQEITDELI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRAMKQWEPRIQEITDELI 120

Qy        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180

Qy        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPFCTLLLVAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPLCTLLLVAG 240
```

```
Qy        241 NETTTNLISNAMYSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NETTTNLISNAMYSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300

Qy        301 GHLIKEGDMVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GHLIKEGDMVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360

Qy        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396
              |||||||||||||||||||||||||||||||||||||
Db        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396


RESULT 3
US-09-869-334B-45
; Sequence 45, Application US/09869334B
; GENERAL INFORMATION:
;  APPLICANT: ENDO, Hirofumi
;  APPLICANT:  MIZOGUCHI, Hiroshi
;  APPLICANT:  OZAKI, Akio
;  APPLICANT:  YONETANI, Yoshiyuki
;  APPLICANT:  HASHIMOTO, Shin-ichi
;  TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
;  FILE REFERENCE: P21289
;  CURRENT APPLICATION NUMBER: US/09/869,334B
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: PCT JP00/00472
;  PRIOR FILING DATE: 2000-01-28
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 396
;   TYPE: PRT
;   ORGANISM: Bacillus subtilis
US-09-869-334B-45

  Query Match             98.3%;  Score 2018;  DB 1;  Length 396;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches  389;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNVLNRRQALPRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60

Qy         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRVMKQWEPRIQEITDELI 120
              |||||||||||||||||||:|||||||||||||||||| ||||||||||||||||||||
Db         61 GDKELFSSCMPQQTSSIGNSIISMDPPKHTKIRSVVNKAFTPRAMKQWEPRIQEITDELI 120

Qy        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180
              ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKFQGRSEFDLVHDYSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180

Qy        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPFCTLLLVAG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPLCTLLLVAG 240

Qy        241 NETTTNLISNAMYSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300
              ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NETTTNLISNAMFSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300

Qy        301 GHLIKEGDMVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GHLIKEGDTVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360

Qy        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396
              |||||||||||||||||||||||||||||||||||||
Db        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396


Search completed: March 31, 2004, 08:08:52
Job time : 0.001 secs
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OM protein - protein search, using sw model

Run on: March 31, 2004, 08:08:52 ; Search time 0.001 Seconds
(without alignments)
470.448 Million cell updates/sec

Title: 2633575
Perfect score: 2052
Sequence: 1 mnvlnrrqalqrallngknk.....sitpiensviyglksfrvkm 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3 seqs, 1188 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : US09869334B.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2052	100.0	396	1	US-09-869-334B-1	Sequence 1, Appli
2	2042	99.5	396	1	US-09-869-334B-42	Sequence 42, Appl
3	2018	98.3	396	1	US-09-869-334B-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-869-334B-1
; Sequence 1, Application US/09869334B
; GENERAL INFORMATION:
; APPLICANT: ENDO, Hirofumi
; APPLICANT: MIZOGUCHI, Hiroshi
; APPLICANT: OZAKI, Akio
; APPLICANT: YONETANI, Yoshiyuki
; APPLICANT: HASHIMOTO, Shin-ichi
; TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
; FILE REFERENCE: P21289
; CURRENT APPLICATION NUMBER: US/09/869,334B
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: PCT JP00/00472
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-869-334B-1

Query Match 100.0%; Score 2052; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60

Qy         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRVMKQWEPRIQEITDELI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRVMKQWEPRIQEITDELI 120

Qy        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180

Qy        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPFCTLLLVAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPFCTLLLVAG 240

Qy        241 NETTTNLISNAMYSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NETTTNLISNAMYSILETPGVYEELRSHPELMPQAVEEALRFRAPAPVLRRIAKRDTEIG 300

Qy        301 GHLIKEGDMVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GHLIKEGDMVLAFVASANRDEAKFDRPHMFDIRRHPNPHIAFGHGIHFCLGAPLARLEAN 360

Qy        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396
              |||||||||||||||||||||||||||||||||||
Db        361 IALTSLISAFPHMECVSITPIENSVIYGLKSFRVKM 396
```

RESULT 2
US-09-869-334B-42
; Sequence 42, Application US/09869334B
; GENERAL INFORMATION:
; APPLICANT: ENDO, Hirofumi
; APPLICANT: MIZOGUCHI, Hiroshi
; APPLICANT: OZAKI, Akio
; APPLICANT: YONETANI, Yoshiyuki
; APPLICANT: HASHIMOTO, Shin-ichi
; TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
; FILE REFERENCE: P21289
; CURRENT APPLICATION NUMBER: US/09/869,334B
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: PCT JP00/00472
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-869-334B-42

Query Match 99.5%; Score 2042; DB 1; Length 396;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 394; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEENQVWSVFLYDDVKKVV 60

Qy         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRVMKQWEPRIQEITDELI 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         61 GDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTPRAMKQWEPRIQEITDELI 120

Qy        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKAWSDLLVSTPKDKSEEAEKAF 180

Qy        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPFCTLLLVAG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        181 LEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAEETGEKLSGEELIPLCTLLLVAG 240
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